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OM protein - protein search, using sw model

Run on: April 3, 2006, 08:26:10 ; Search time 78.5658 Seconds
(without alignments)
3345.152 Million cell updates/sec

Title: US-10-715-667-21

Perfect score: 3334

Sequence: 1 MNQYTIQMDAVIALYILFSM.....TYFPQNIHSHNRISLEK 629

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 100 summaries

Database : Published Applications AA Main:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3334	100.0	629	3	US-09-972-708-21
2	3334	100.0	629	4	US-10-105-930-10
3	3334	100.0	629	3	US-10-715-667-21
4	3314	99.4	629	3	US-09-853-180-2
5	3314	99.4	629	5	US-10-797-157-6
6	3314	99.4	629	5	US-10-720-026-2
7	3314	99.4	629	5	US-10-667-289-2
8	3314	99.4	629	5	US-10-667-290-2
9	3312	99.3	629	4	US-10-105-930-6
10	2972	89.1	565	3	US-09-972-708-23
11	2972	89.1	565	4	US-10-715-667-23
12	2278.5	68.3	644	3	US-09-972-708-27
13	2278.5	68.3	644	4	US-10-715-667-27
14	2212	66.3	428	4	US-10-105-930-8
15	2195	65.8	428	4	US-10-105-930-4
16	2037	61.1	384	3	US-09-972-708-26
17	2037	61.1	384	4	US-10-247-463-2
18	2037	61.1	384	4	US-10-715-667-26
19	2037	61.1	384	6	US-11-016-106-2
20	1888	56.6	356	3	US-09-972-708-25
21	1888	56.6	356	4	US-10-715-667-25
22	1715	51.4	337	4	US-10-105-930-2
23	1020.5	30.6	344	3	US-09-972-708-16
24	1020.5	30.6	344	4	US-10-715-667-16
25	293	8.8	52	4	US-10-105-930-24
26	262	7.9	46	4	US-10-105-930-28
27	232	7.0	951	3	US-09-313-942-9

28	232	7.0	951	3	US-09-935-868-9	Sequence 9, Appl1
29	232	7.0	951	4	US-10-287-025-9	Sequence 9, Appl1
30	232	7.0	951	4	US-10-282-162-9	Sequence 9, Appl1
31	232	7.0	951	6	US-11-134-114-9	Sequence 9, Appl1
32	227	6.8	861	4	US-10-398-666-12	Sequence 12, Appl1
33	224	6.7	39	4	US-10-105-930-27	Sequence 27, Appl1
34	222	6.7	862	3	US-09-853-180-5	Sequence 5, Appl1
35	222	6.7	862	5	US-10-797-157-7	Sequence 7, Appl1
36	222	6.7	862	5	US-10-370-715B-68	Sequence 68, Appl1
37	222	6.7	862	5	US-10-720-026-4	Sequence 4, Appl1
38	222	6.7	862	5	US-10-667-289-4	Sequence 4, Appl1
39	222	6.7	862	5	US-10-667-290-4	Sequence 4, Appl1
40	220	6.6	859	3	US-09-313-942-7	Sequence 7, Appl1
41	220	6.6	859	3	US-09-935-868-7	Sequence 7, Appl1
42	220	6.6	859	4	US-10-287-035-7	Sequence 7, Appl1
43	220	6.6	859	4	US-10-282-162-7	Sequence 7, Appl1
44	220	6.6	859	6	US-11-134-114-7	Sequence 7, Appl1
45	215	6.4	918	3	US-09-853-180-4	Sequence 4, Appl1
46	215	6.4	918	3	US-09-972-708-8	Sequence 8, Appl1
47	215	6.4	918	3	US-09-829-472A-9	Sequence 9, Appl1
48	215	6.4	918	4	US-10-177-293-230	Sequence 230, Appl1
49	215	6.4	918	4	US-10-295-027-74	Sequence 32, Appl1
50	215	6.4	918	4	US-10-058-270A-32	Sequence 32, Appl1
51	215	6.4	918	4	US-10-715-667-8	Sequence 8, Appl1
52	215	6.4	918	5	US-10-720-026-3	Sequence 3, Appl1
53	215	6.4	918	5	US-10-667-289-3	Sequence 3, Appl1
54	215	6.4	918	5	US-10-667-290-3	Sequence 3, Appl1
55	214	6.4	918	6	US-11-067-251-5	Sequence 5, Appl1
56	213	6.4	332	3	US-09-313-942-10	Sequence 10, Appl1
57	213	6.4	332	3	US-09-935-868-10	Sequence 10, Appl1
58	213	6.4	332	4	US-10-287-035-10	Sequence 10, Appl1
59	213	6.4	332	4	US-10-282-162-10	Sequence 10, Appl1
60	213	6.4	332	6	US-11-134-114-10	Sequence 10, Appl1
61	213	6.4	918	5	US-10-850-270-6	Sequence 6, Appl1
62	212	6.4	708	4	US-10-313-135-2	Sequence 2, Appl1
63	210	6.3	1158	3	US-09-313-942-26	Sequence 26, Appl1
64	210	6.3	1158	3	US-09-935-868-26	Sequence 26, Appl1
65	210	6.3	1158	4	US-10-287-035-26	Sequence 26, Appl1
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67	210	6.3	1158	6	US-11-134-114-26	Sequence 26, Appl1
68	210	6.3	1168	3	US-09-313-942-24	Sequence 24, Appl1
69	210	6.3	1168	3	US-09-935-868-24	Sequence 24, Appl1
70	210	6.3	1168	4	US-10-287-035-24	Sequence 24, Appl1
71	210	6.3	1168	4	US-10-282-162-24	Sequence 24, Appl1
72	210	6.3	1168	6	US-11-134-114-24	Sequence 24, Appl1
73	208	6.2	329	5	US-10-755-889-426	Sequence 426, Appl1
74	208	6.2	329	5	US-10-884-043-1	Sequence 1, Appl1
75	208	6.2	807	4	US-10-311-473-12	Sequence 12, Appl1
76	207.5	6.2	488	4	US-10-079-625-5	Sequence 5, Appl1
77	197	5.9	34	4	US-10-105-930-29	Sequence 29, Appl1
78	196	5.9	36	3	US-09-864-761-489A8	Sequence 489A8, A
79	194	5.8	1097	3	US-09-972-708-6	Sequence 6, Appl1
80	194	5.8	1097	4	US-10-715-667-6	Sequence 6, Appl1
81	194	5.8	1119	4	US-10-276-774-2690	Sequence 2690, Appl1
82	192.5	5.8	652	3	US-09-972-708-14	Sequence 14, Appl1
83	192.5	5.8	652	4	US-10-006-265-2	Sequence 2, Appl1
84	192.5	5.8	652	4	US-10-715-667-14	Sequence 14, Appl1
85	191.5	5.7	649	3	US-09-892-949-46	Sequence 46, Appl1
86	191.5	5.7	649	4	US-10-351-157-109	Sequence 109, Appl1
87	191.5	5.7	649	4	US-10-772-531-46	Sequence 46, Appl1
88	191.5	5.7	649	5	US-10-982-555-46	Sequence 46, Appl1
89	191.5	5.7	662	3	US-09-972-708-15	Sequence 15, Appl1
90	191.5	5.7	662	3	US-09-892-949-54	Sequence 54, Appl1
91	191.5	5.7	662	4	US-10-006-265-17	Sequence 17, Appl1
92	191.5	5.7	662	4	US-10-351-157-5	Sequence 5, Appl1
93	191.5	5.7	662	4	US-10-352-554-5	Sequence 5, Appl1
94	191.5	5.7	662	4	US-10-772-531-54	Sequence 54, Appl1
95	191.5	5.7	662	4	US-10-715-667-15	Sequence 15, Appl1
96	191.5	5.7	662	5	US-10-982-555-54	Sequence 54, Appl1
97	191.5	5.7	732	3	US-09-892-949-2	Sequence 2, Appl1
98	191.5	5.7	732	4	US-10-351-157-111	Sequence 111, Appl1
99	191.5	5.7	732	4	US-10-772-531-2	Sequence 2, Appl1
100	191.5	5.7	732	5	US-10-982-555-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1
US-09-972-708-21
; Sequence 21, Application US/09972708
; Publication No. US20030059871A1
GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Cosman, David J.
; APPLICANT: Mosley, Bruce A.
; APPLICANT: Bird, Timothy A.
; APPLICANT: Dubose, Robert F.
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: HEMATOPOIETIN RECEPTORS HPR1 AND HPR2
; FILE REFERENCE: 3160-B
; CURRENT APPLICATION NUMBER: US/09/972,708
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 21
; LENGTH: 629
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-708-21

Query Match 100.0%; Score 3334; DB 3; Length 629;
Best Local Similarity 100.0%; Pred. No. 1.3e-242;
Matches 629; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNQVITQMDAVIALYILFSWCHGGITNINCSGHIWVEBATTFKMGMINISYCOALIKNCQ 60
DB 1 MNQVITQMDAVIALYILFSWCHGGITNINCSGHIWVEBATTFKMGMINISYCOALIKNCQ 60
QY 61 PKLHFYKNGIKERQITRINKTARLWKYKFLBPHASMYCTACBCKPFOETLIGCKDIS 120
DB 61 PKLHFYKNGIKERQITRINKTARLWKYKFLBPHASMYCTACBCKPFOETLIGCKDIS 120
QY 121 SGYPDIPDEVYCVIYEVSGNMTCTWNAKLTYYIDTKYVHVKSLETEBEOQYLTSSYIN 180
DB 121 SGYPDIPDEVYCVIYEVSGNMTCTWNAKLTYYIDTKYVHVKSLETEBEOQYLTSSYIN 180
QY 161 ISTDSLQGGKTYLVWQAAANALGMBESKQLOIHDDIYIPSAAVISRAETINATVPKTI 240
DB 161 ISTDSLQGGKTYLVWQAAANALGMBESKQLOIHDDIYIPSAAVISRAETINATVPKTI 240
QY 241 YNDSQTTIEKVSCEMRKYATNQTNVKEFDNFTYVOOSEFYLBEPNIIKYVQVRCQETG 300
DB 241 YNDSQTTIEKVSCEMRKYATNQTNVKEFDNFTYVOOSEFYLBEPNIIKYVQVRCQETG 300
QY 301 KRYWQPMWSLFFHKTPETVPOVTSKAFQHDITWNSGLTVASISTGHLTSDNRGDIGLLGM 360
DB 301 KRYWQPMWSLFFHKTPETVPOVTSKAFQHDITWNSGLTVASISTGHLTSDNRGDIGLLGM 360
QY 361 IYFAVWLSTLSLIGIFNRSFRGTGIRKRIILLIPKMLYEDI PMKKSNNVVKMLQENSELMN 420
DB 361 IYFAVWLSTLSLIGIFNRSFRGTGIRKRIILLIPKMLYEDI PMKKSNNVVKMLQENSELMN 420
QY 421 NNSSEOVLYVDMPTIEIKEIFIPEHKPTDYKKENTGPLETRDY PONSLEPNTTVYYIPDL 480
DB 421 NNSSEOVLYVDMPTIEIKEIFIPEHKPTDYKKENTGPLETRDY PONSLEPNTTVYYIPDL 480
QY 481 NTGYKPOISNPLPEGSHLSNNNEITSLLTKPVDSDSGNNPRLQKHPAFASVS VNSL 540
DB 481 NTGYKPOISNPLPEGSHLSNNNEITSLLTKPVDSDSGNNPRLQKHPAFASVS VNSL 540
QY 541 SNTITLGEISLILNCGECSSPDIONSVEBETTMLENDSPESTIPEQTLIPBEPVSCIGI 600
DB 541 SNTITLGEISLILNCGECSSPDIONSVEBETTMLENDSPESTIPEQTLIPBEPVSCIGI 600
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DB 601 VNEBLPSINTYFPQNILBSHFNRISLBRK 629

RESULT 2
US-10-105-930-10
; Sequence 10, Application US/10105930
; Publication No. US2003009018A1
GENERAL INFORMATION:
; APPLICANT: Maeda, Masatsugu
; APPLICANT: Yaguchi, No. US2003009018A1iko
; TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR12
; FILE REFERENCE: 06501-105US1
; CURRENT APPLICATION NUMBER: US/10/105,930
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: PCT/JP00/06654
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: JP 2000-240397
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: JP 11-273358
; PRIOR FILING DATE: 1999-09-27
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 629
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-105-930-10

Query Match 100.0%; Score 3334; DB 4; Length 629;
Best Local Similarity 100.0%; Pred. No. 1.3e-242;
Matches 629; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNQVITQMDAVIALYILFSWCHGGITNINCSGHIWVEBATTFKMGMINISYCOALIKNCQ 60
DB 1 MNQVITQMDAVIALYILFSWCHGGITNINCSGHIWVEBATTFKMGMINISYCOALIKNCQ 60
QY 61 PKLHFYKNGIKERQITRINKTARLWKYKFLBPHASMYCTACBCKPFOETLIGCKDIS 120
DB 61 PKLHFYKNGIKERQITRINKTARLWKYKFLBPHASMYCTACBCKPFOETLIGCKDIS 120
QY 121 SGYPDIPDEVYCVIYEVSGNMTCTWNAKLTYYIDTKYVHVKSLETEBEOQYLTSSYIN 180
DB 121 SGYPDIPDEVYCVIYEVSGNMTCTWNAKLTYYIDTKYVHVKSLETEBEOQYLTSSYIN 180
QY 161 ISTDSLQGGKTYLVWQAAANALGMBESKQLOIHDDIYIPSAAVISRAETINATVPKTI 240
DB 161 ISTDSLQGGKTYLVWQAAANALGMBESKQLOIHDDIYIPSAAVISRAETINATVPKTI 240
QY 241 YNDSQTTIEKVSCEMRKYATNQTNVKEFDNFTYVOOSEFYLBEPNIIKYVQVRCQETG 300
DB 241 YNDSQTTIEKVSCEMRKYATNQTNVKEFDNFTYVOOSEFYLBEPNIIKYVQVRCQETG 300
QY 301 KRYWQPMWSLFFHKTPETVPOVTSKAFQHDITWNSGLTVASISTGHLTSDNRGDIGLLGM 360
DB 301 KRYWQPMWSLFFHKTPETVPOVTSKAFQHDITWNSGLTVASISTGHLTSDNRGDIGLLGM 360
QY 361 IYFAVWLSTLSLIGIFNRSFRGTGIRKRIILLIPKMLYEDI PMKKSNNVVKMLQENSELMN 420
DB 361 IYFAVWLSTLSLIGIFNRSFRGTGIRKRIILLIPKMLYEDI PMKKSNNVVKMLQENSELMN 420
QY 421 NNSSEOVLYVDMPTIEIKEIFIPEHKPTDYKKENTGPLETRDY PONSLEPNTTVYYIPDL 480
DB 421 NNSSEOVLYVDMPTIEIKEIFIPEHKPTDYKKENTGPLETRDY PONSLEPNTTVYYIPDL 480
QY 481 NTGYKPOISNPLPEGSHLSNNNEITSLLTKPVDSDSGNNPRLQKHPAFASVS VNSL 540
DB 481 NTGYKPOISNPLPEGSHLSNNNEITSLLTKPVDSDSGNNPRLQKHPAFASVS VNSL 540
QY 541 SNTITLGEISLILNCGECSSPDIONSVEBETTMLENDSPESTIPEQTLIPBEPVSCIGI 600
DB 541 SNTITLGEISLILNCGECSSPDIONSVEBETTMLENDSPESTIPEQTLIPBEPVSCIGI 600

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OM protein - protein search, using sw model

Run on: April 3, 2006, 08:26:10 ; Search time 44.4665 Seconds
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3345.152 Million cell updates/sec

Title: US-10-715-667-25

Perfect score: 1934

Sequence: 1 MNQYTIQMDAVIALYILFSW.....TVASISGHLISGLKEGSGYC 356

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Published Applications AA Main:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

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SUMMARIES

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1	1934	100.0	356	3	US-09-972-708-25
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4	1888	97.6	629	3	US-09-972-708-21
5	1888	97.6	629	4	US-10-105-930-10
6	1888	97.6	629	4	US-10-715-667-21
7	1881	97.3	384	3	US-09-972-708-26
8	1881	97.3	384	4	US-10-247-463-2
9	1881	97.3	384	4	US-10-715-667-26
10	1881	97.3	384	6	US-11-016-106-2
11	1871	96.7	428	4	US-10-105-930-4
12	1871	96.7	629	4	US-10-105-930-6
13	1868	96.6	629	3	US-09-853-180-2
14	1868	96.6	629	5	US-10-720-026-2
15	1868	96.6	629	5	US-10-720-026-2
16	1868	96.6	629	5	US-10-667-289-2
17	1868	96.6	629	5	US-10-667-289-2
18	1732	89.6	565	3	US-09-972-708-23
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29	222	11.5	862	3	US-09-853-180-5	Sequence 5, Appl
30	222	11.5	862	5	US-10-797-157-7	Sequence 7, Appl
31	222	11.5	862	5	US-10-370-715B-68	Sequence 68, Appl
32	222	11.5	862	5	US-10-720-026-4	Sequence 4, Appl
33	222	11.5	862	5	US-10-667-289-4	Sequence 4, Appl
34	222	11.5	862	5	US-10-667-290-4	Sequence 4, Appl
35	215.5	11.1	859	3	US-09-313-942-7	Sequence 7, Appl
36	215.5	11.1	859	3	US-09-313-942-7	Sequence 7, Appl
37	215.5	11.1	859	4	US-10-287-035-7	Sequence 7, Appl
38	215.5	11.1	859	4	US-10-287-162-7	Sequence 7, Appl
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41	215.5	11.1	951	3	US-09-313-868-9	Sequence 9, Appl
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46	213	11.0	332	3	US-09-935-868-10	Sequence 10, Appl
47	213	11.0	332	4	US-10-287-035-10	Sequence 10, Appl
48	213	11.0	332	6	US-11-134-114-10	Sequence 10, Appl
49	212.5	11.0	918	4	US-10-287-162-10	Sequence 10, Appl
50	212.5	11.0	918	3	US-09-853-180-4	Sequence 4, Appl
51	212.5	11.0	918	3	US-09-972-708-8	Sequence 8, Appl
52	212.5	11.0	918	3	US-09-829-472A-9	Sequence 9, Appl
53	212.5	11.0	918	4	US-10-177-293-230	Sequence 230, Appl
54	212.5	11.0	918	4	US-10-295-027-74	Sequence 74, Appl
55	212.5	11.0	918	4	US-10-058-270A-32	Sequence 32, Appl
56	212.5	11.0	918	4	US-10-715-667-8	Sequence 8, Appl
57	212.5	11.0	918	5	US-10-720-026-3	Sequence 3, Appl
58	212.5	11.0	918	5	US-10-850-270-6	Sequence 6, Appl
59	212.5	11.0	918	5	US-10-667-289-3	Sequence 3, Appl
60	212.5	11.0	918	5	US-10-667-290-3	Sequence 3, Appl
61	211.5	10.9	708	4	US-10-313-135-2	Sequence 2, Appl
62	211.5	10.9	918	6	US-11-067-251-5	Sequence 5, Appl
63	208	10.8	329	4	US-10-755-889-426	Sequence 426, Appl
64	208	10.8	329	5	US-10-884-043-1	Sequence 1, Appl
65	207.5	10.7	488	4	US-10-079-625-5	Sequence 5, Appl
66	207.5	10.7	807	4	US-10-311-473-12	Sequence 12, Appl
67	207.5	10.7	1158	3	US-09-313-942-26	Sequence 26, Appl
68	207.5	10.7	1158	4	US-09-935-868-26	Sequence 26, Appl
69	207.5	10.7	1158	4	US-10-287-035-26	Sequence 26, Appl
70	207.5	10.7	1158	4	US-10-287-162-26	Sequence 26, Appl
71	207.5	10.7	1158	6	US-11-134-114-26	Sequence 26, Appl
72	207.5	10.7	1168	3	US-09-313-942-24	Sequence 24, Appl
73	207.5	10.7	1168	3	US-09-935-868-24	Sequence 24, Appl
74	207.5	10.7	1168	4	US-10-287-035-24	Sequence 24, Appl
75	207.5	10.7	1168	4	US-10-282-162-24	Sequence 24, Appl
76	207.5	10.7	1168	6	US-11-134-114-24	Sequence 24, Appl
77	197	10.2	34	4	US-10-105-930-29	Sequence 29, Appl
78	196	10.1	36	3	US-09-864-761-48948	Sequence 48948, A
79	186.5	9.6	837	3	US-10-659-295-35	Sequence 35, Appl
80	186.5	9.6	837	5	US-10-880-101A-35	Sequence 35, Appl
81	182	9.4	1097	3	US-09-972-708-6	Sequence 6, Appl
82	182	9.4	1097	4	US-10-715-667-6	Sequence 6, Appl
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84	170	8.8	836	3	US-09-972-708-9	Sequence 9, Appl
85	170	8.8	836	4	US-10-659-295-34	Sequence 34, Appl
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87	170	8.8	836	5	US-10-880-101A-34	Sequence 34, Appl
88	167.5	8.7	603	4	US-10-071-962-27	Sequence 27, Appl
89	167	8.6	385	3	US-09-880-578-19	Sequence 19, Appl
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91	167	8.6	405	4	US-10-074-901-2	Sequence 2, Appl
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93	167	8.6	425	3	US-09-880-578-6	Sequence 6, Appl
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95	163.5	8.5	303	3	US-09-880-578-21	Sequence 21, Appl
96	163.5	8.5	389	3	US-09-880-578-24	Sequence 24, Appl
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98	163.5	8.5	389	3	US-09-880-578-29	Sequence 29, Appl
99	163.5	8.5	422	3	US-09-880-578-2	Sequence 2, Appl
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ALIGNMENTS

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; Sequence 25, Application US/09972708
; Publication No. US20030059871A1
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Cosman, David J.
; APPLICANT: Mosley, Bruce A.
; APPLICANT: Bird, Timothy A.
; APPLICANT: Dubose, Robert F.
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: HEMATOPOIETIN RECEPTORS HPRI AND HPR2
; FILE REFERENCE: 3160-B
; CURRENT APPLICATION NUMBER: US/09/972,708
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 356
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-708-25
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DB 121 SGYPDIPDEVTCVYIYERSGMNTCTWNAKGLTYIDTKYVHVKSLETEBEOQYLTSSYIN 180
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DB 181 ISTSLQGGKKYLVWVOAANALGMESKQLOIHLDDIYIPSAVYSRAETINATVPKTI 240
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DB 301 KRYWQPMSSLPFHKTPEVTPVQVTSKAFQHDWTNNSGLTYASISTGHLTSGLKRGSYC 356
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US-10-715-667-25
; Sequence 25, Application US/10715667
; Publication No. US20040152161A1
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Cosman, David J.
; APPLICANT: Mosley, Bruce A.
; APPLICANT: Bird, Timothy A.
; APPLICANT: Dubose, Robert F.
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: HEMATOPOIETIN RECEPTORS HPRI AND HPR2
; FILE REFERENCE: 3160-B
; CURRENT APPLICATION NUMBER: US/10/715,667
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: US/09/972,708
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; PRIOR FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 356
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-715-667-25
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Query Match      100.0%; Score 1934; DB 4; Length 356;
Best Local Similarity 100.0%; Pred. No. 3.8e-157;
Matches 356; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 61 PRKLHFYKNGIKERFOITRIKNTARLWYKNFLBPHASMYCTABCPKHFQETLIGCKDIS 120
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DB 121 SGYPDIPDEVTCVYIYERSGMNTCTWNAKGLTYIDTKYVHVKSLETEBEOQYLTSSYIN 180
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DB 181 ISTSLQGGKKYLVWVOAANALGMESKQLOIHLDDIYIPSAVYSRAETINATVPKTI 240
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DB 301 KRYWQPMSSLPFHKTPEVTPVQVTSKAFQHDWTNNSGLTYASISTGHLTSGLKRGSYC 356
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US-10-105-930-8
; Sequence 8, Application US/10105930
; Publication No. US20030009018A1
; GENERAL INFORMATION:
; APPLICANT: Maeda, Masatoshu
; APPLICANT: Yasuchi, No. US20030009018A1ko
; TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR12
; FILE REFERENCE: 06501-105051
; CURRENT APPLICATION NUMBER: US/10/105,930
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: PCT/JP00/06654
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: JP 2000-240397
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: JP 11-273358
; PRIOR FILING DATE: 1999-09-27
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-105-930-8
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Best Local Similarity 100.0%; Pred. No. 4.3e-153;
Matches 348; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MNOVTIQMDAVIALYILFSWCHGGITNINSGHIMVEBATTIFKMGMINISYCOAALIKNCQ 60
QY 61 PRKLHFYKNGIKERFOITRIKNTARLWYKNFLBPHASMYCTABCPKHFQETLIGCKDIS 120
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OM protein - protein search, using sw model

Run on: April 3, 2006, 08:22:56 ; Search time 176.536 Seconds
(without alignment)
2513.799 Million cell updates/sec

Title: US-10-715-667-21

Perfect score: 3334

Sequence: 1 MNQVITQMDAVIALYILFSW.....TYFPQNIUESHPNRISLEK 629

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Uniprot 05.80:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	3327	99.8	629	2	Q8NFG9_HUMAN
3	3120	93.6	629	2	Q4VGP6_HUMAN
4	2282.5	68.5	644	2	Q8K4B4_MOUSE
5	1948	58.4	675	2	Q4VGP4_HUMAN
6	1895	56.8	390	2	Q5VWK7_HUMAN
7	1888	56.6	391	2	Q5VWK7_HUMAN
8	1674	50.2	320	2	Q4VGP1_HUMAN
9	1655	49.6	320	2	Q4VGP3_HUMAN
10	1271	38.1	264	2	Q4VGP2_HUMAN
11	1175	35.2	227	2	Q8IWB4_HUMAN
12	705	22.1	138	2	Q4VGP5_HUMAN
13	335.5	10.1	869	2	Q5GR16_CHICK
14	281.5	8.4	918	2	Q9W6U9_CHICK
15	277	8.3	554	2	Q6UAN2_TETNG
16	261.5	7.8	917	1	IL6RB_MOUSE
17	261.5	7.8	917	2	Q6PD19_MOUSE
18	256.5	7.7	874	1	IL1R2_MOUSE
19	253.5	7.6	861	1	IL1R2_BOVIN
20	246.5	7.4	881	2	O57519_XENLA
21	240.5	7.4	1010	2	Q7TQ89_RAT
22	240.5	7.2	813	2	Q6UAN1_TETNG
23	231.5	6.9	857	2	O5FC04_HUMAN
24	230.5	6.9	918	1	IL6RB_RAT
25	230	6.9	858	2	Q4QYC6_CANFA
26	223	6.7	861	1	IL1R2_PIG
27	222	6.7	862	1	IL1R2_HUMAN
28	222	6.7	862	2	O5VWK8_HUMAN
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30	215	6.4	918	1	IL6RB_HUMAN
31	202	6.1	622	2	Q5RAWO_PONPY

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34	195	5.8	764	2	Q6EBC4_HUMAN
35	194	5.8	1097	1	ILFR_HUMAN
36	192	5.7	739	2	Q4T141_TETNG
37	191.5	5.7	649	2	Q6EBC6_HUMAN
38	191.5	5.7	662	2	Q6EBC3_HUMAN
39	191.5	5.7	732	2	Q8N117_HUMAN
40	191	5.7	622	1	PRLR_HUMAN
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43	187	5.6	1097	2	Q5XNR9_CANFA
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55	166	5.0	376	2	Q96P35_HUMAN
56	166	5.0	884	2	Q6UAM6_TETNG
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58	164.5	4.9	425	1	C5R1F1_MOUSE
59	163	4.9	609	2	Q51SE1_CYPCA
60	163	4.9	831	1	PRLR_CHICK
61	163	4.9	1093	2	Q70535_RAT
62	162.5	4.9	422	1	C5R1F1_HUMAN
63	161.5	4.8	349	2	Q9UHU5_HUMAN
64	161.5	4.8	604	2	Q8Q354_CYPCA
65	161	4.8	831	2	Q6GDA0_CHICK
66	160.5	4.8	608	1	GHR_CHICK
67	158.5	4.8	600	2	Q9PTP0_CARAU
68	158	4.7	324	2	Q6EBC5_HUMAN
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71	156.5	4.7	581	1	PRLR_RAT
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82	153.5	4.6	831	1	PRLR_MELGA
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84	153	4.6	229	2	Q5VWK6_HUMAN
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87	151.5	4.5	1148	2	Q91BA7_CHICK
88	151	4.5	581	1	PRLR_CEREL
89	151	4.5	608	1	PRLR_MOUSE
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92	150.5	4.5	1166	2	Q4W810_CANFA
93	149.5	4.5	557	2	Q50EX8_SPAU
94	149.5	4.5	583	2	Q50H40_SPAU
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Q6EBC3	HUMAN	Q6EBC3	HUMAN
Q8N117	HUMAN	Q8N117	HUMAN
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Q6UAQ5	TETNG	Q6UAQ5	TETNG
Q5XNR9	CANFA	Q5XNR9	CANFA
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Q9N0J7	CALJA	Q9N0J7	CALJA
Q865V4	CEBAP	Q865V4	CEBAP
Q6UA22	BRARE	Q6UA22	BRARE
Q51072	BOVIN	Q51072	BOVIN
ILFR	BOVIN	ILFR	BOVIN
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Q96P35	HUMAN	Q96P35	HUMAN
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Q616F7	EUBMA	Q616F7	EUBMA
P05710	OVIS ARIES	P05710	OVIS ARIES
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Q85501	OROECHROMIS	Q85501	OROECHROMIS
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Q8K5B1	MUS MUSCULI	Q8K5B1	MUS MUSCULI
Q91094	MELEAGRIS G	Q91094	MELEAGRIS G
Q02671	SUS SCROFA	Q02671	SUS SCROFA
Q5VWK6	HUMAN	Q5VWK6	HUMAN
P48357	HOMO SAPIEN	P48357	HOMO SAPIEN
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Q91BA7	GALLUS GALLI	Q91BA7	GALLUS GALLI
Q28333	CERVUS ELAP	Q28333	CERVUS ELAP
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Q9JUZ1	MUS MUSCULI	Q9JUZ1	MUS MUSCULI
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DT 01-FEB-2005 (TREMBlrel. 29, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OC NCBI_TaxID=9606;
RN [1]
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RA Hall R.;
RL Submitted (MAY-2005) to the EMBL/Genbank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Davidson C.;
RL Submitted (MAY-2005) to the EMBL/Genbank/DBJ databases.
DR EMBL; AL389925; CAH70406.1; -; Genomic DNA.
DR EMBL; AL109843; CAI22678.1; -; Genomic DNA.
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DR EMBL; AL389925; CAI22678.1; JOINED; Genomic DNA.
DR HGNC; HGNC:19100; IL23R.
DR GO; GO:0016021; C:Integral to membrane, IEA.
DR GO; GO:0004872; F:Receptor activity, IEA.
DR InterPro; IPR003961; FN_III.
DR Pfam; PF00041; fn3; 1.
DR PROSITE; PS50853; FN3; 2.
DR Receptor; Repeat; Transmembrane.
DR KJ SEQUENCE 629 AA; 7172 MW; AC63C98B81ABF05 CRC64;
SQ
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Best Local Similarity 100.0%; Pred. No. 5,76-212;
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DT 01-OCT-2002 (TREMBlrel. 22, Created)
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DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
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RA MEDLINE=22018152; PubMed=12023369;
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RA Pfanz S., Zhang R., Singh K.P., Vega F., To W., Wagner J.,
RA O'Farrell A.-M., McClanahan T., Zurawski S., Hannum C., Gorman D.,
RA Renick D.M., Kastelein R.A., de Waal Malefyt R., Moore K.W.; of IL-
RT "A receptor for the heterodimeric cytokine IL-23 is composed of IL-
RL J. Immunol. 168:5699-5708(2002).
DR EMBL; AF61422; AAM44229.1; -; mRNA.
DR HSSP; P16471; 1BP3.
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DR HGNC; HGNC:19100; IL23R.
DR GO; GO:0004872; F:Receptor activity, IEA.
DR InterPro; IPR003961; FN_III.
DR Pfam; PF00041; fn3; 1.
DR SMART; SMO0060; FN3; 1.
DR PROSITE; PS50853; FN3; 2.
DR Receptor.
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Best Local Similarity 99.8%; Pred. No. 1,66-211;
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GenCore version 5.1.7
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Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	232	7.0	951	2	US-09-313-942-9
3	232	7.0	951	2	US-10-282-162-9
4	222	6.7	862	1	US-08-685-118-2
5	222	6.7	862	1	US-08-915-495-2
6	222	6.7	862	1	US-08-914-520-2
7	222	6.7	862	2	US-09-853-180B-4
8	222	6.7	864	2	US-09-949-016-7758
9	220	6.6	859	2	US-09-313-942-7
10	220	6.6	859	2	US-10-282-162-7
11	217	6.5	918	1	US-08-825-558-6
12	217	6.5	918	2	US-09-312-611-6
13	215	6.4	918	2	US-09-853-180B-3
14	215	6.4	918	2	US-09-949-002-333
15	214	6.4	937	2	US-09-949-002-536
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18	213	6.4	658	1	US-08-825-558-4
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86	160.5	4.8	389	2	US-09-071-224-31	Sequence 31, App1
87	160.5	4.8	389	2	US-09-521-335-13	Sequence 13, App1
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ALIGNMENTS

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; Sequence 2, Application US/09853180B
; Patent No. 6756481
; GENERAL INFORMATION:
; APPLICANT: Chirica, Madaline
; APPLICANT: Parham, Christi L.
; APPLICANT: Kastelein, Robert A.
; APPLICANT: Moore, Kevin W.
; TITLE OF INVENTION: Mammalian Receptor Proteins; Related Reagents and Methods.
; FILE REFERENCE: DKO1074
; CURRENT APPLICATION NUMBER: US/09/853,180B
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 60/203,426
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 629
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (-21)..(-21)
; OTHER INFORMATION: The 'Xaa' at location -21 stands for Gln, or His.
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; NAME/KEY: misc_feature
; LOCATION: (126)..(126)
; OTHER INFORMATION: The 'Xaa' at location 126 stands for Gly, or Arg.
US-09-853-180B-2

Query Match          99.4%; Score 3314; DB 2; Length 629;
Best Local Similarity 99.5%; Pred. No. 2.4e-290;
Matches 626; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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RESULT 2
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; Sequence 9, Application US/09313942
; Patent No. 6472179
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-A
; CURRENT APPLICATION NUMBER: US/09/313,942
; CURRENT FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 951
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-313-942-9

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 3, 2006, 08:22:41 ; Search time 60.2709 Seconds
(without alignments)
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Title: US-10-715-667-25
Perfect score: 1934
Sequence: 1 MNQVITQMAVIALYILFSW.....TVASISTGHTSLKAGSYC 356

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : A_Geneseq.21.*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1934	100.0	356	5	AAE24035 Human hae
2	1888	97.6	428	4	AAE24035 Human hae
3	1888	97.6	629	4	AAE24035 Human hae
4	1888	97.6	629	5	AAE24035 Human hae
5	1881	97.3	384	4	AAE24035 Human hae
6	1881	97.3	384	5	AAE24035 Human hae
7	1881	97.3	384	5	AAE24035 Human hae
8	1881	97.3	384	5	AAE24035 Human hae
9	1871	96.7	428	4	AAE24035 Human hae
10	1871	96.7	428	4	AAE24035 Human hae
11	1868	96.6	629	5	AAE24035 Human hae
12	1868	96.6	629	5	AAE24035 Human hae
13	1868	96.6	629	5	AAE24035 Human hae
14	1732	89.7	565	5	AAE24035 Human hae
15	1732	89.7	565	5	AAE24035 Human hae
16	1417.5	73.3	644	5	AAE24035 Human hae
17	1020.5	52.8	344	5	AAE24035 Human hae
18	261.5	13.5	917	3	AAE24035 Human hae
19	261.5	13.5	917	3	AAE24035 Human hae
20	261.5	13.5	917	3	AAE24035 Human hae
21	230.5	11.9	918	8	AAE24035 Human hae
22	230.5	11.9	918	8	AAE24035 Human hae
23	227	11.7	861	5	AAE24035 Human hae
24	227	11.7	861	5	AAE24035 Human hae

25	222	11.5	862	2	AAW12771 Human int
26	222	11.5	862	7	ADP39704 Human int
27	222	11.5	862	7	ADP39704 Human int
28	222	11.5	862	8	ADP39704 Human int
29	222	11.5	862	8	ADP39704 Human int
30	222	11.5	862	8	ADP39704 Human int
31	222	11.5	862	8	ADP39704 Human int
32	222	11.5	862	8	ADP39704 Human int
33	222	11.5	862	9	ADP39704 Human int
34	222	11.5	862	9	ADP39704 Human int
35	215.5	11.1	727	3	AAE21092 Human IL-
36	215.5	11.1	727	3	AAE21092 Human IL-
37	215.5	11.1	859	3	AAE21092 Human IL-
38	215.5	11.1	859	3	AAE21092 Human IL-
39	215.5	11.1	859	3	AAE21092 Human IL-
40	215.5	11.1	859	3	AAE21092 Human IL-
41	215.5	11.1	859	3	AAE21092 Human IL-
42	215.5	11.1	859	3	AAE21092 Human IL-
43	215.5	11.1	859	3	AAE21092 Human IL-
44	213	11.0	332	2	AAW0799 Human gp1
45	213	11.0	332	2	AAW0799 Human gp1
46	213	11.0	332	2	AAW0799 Human gp1
47	212.5	11.0	658	2	AAE21092 Human IL-
48	212.5	11.0	658	2	AAE21092 Human IL-
49	212.5	11.0	658	2	AAE21092 Human IL-
50	212.5	11.0	658	2	AAE21092 Human IL-
51	212.5	11.0	658	2	AAE21092 Human IL-
52	212.5	11.0	658	2	AAE21092 Human IL-
53	212.5	11.0	658	2	AAE21092 Human IL-
54	212.5	11.0	658	2	AAE21092 Human IL-
55	212.5	11.0	658	2	AAE21092 Human IL-
56	212.5	11.0	658	2	AAE21092 Human IL-
57	212.5	11.0	658	2	AAE21092 Human IL-
58	212.5	11.0	658	2	AAE21092 Human IL-
59	211.5	10.9	708	2	AAE21092 Human IL-
60	211.5	10.9	708	2	AAE21092 Human IL-
61	211.5	10.9	708	2	AAE21092 Human IL-
62	211.5	10.9	708	2	AAE21092 Human IL-
63	208	10.8	329	8	AAE21092 Human IL-
64	208	10.8	329	8	AAE21092 Human IL-
65	208	10.8	329	8	AAE21092 Human IL-
66	207.5	10.7	488	5	AAE21092 Human IL-
67	207.5	10.7	488	5	AAE21092 Human IL-
68	207.5	10.7	488	5	AAE21092 Human IL-
69	207.5	10.7	488	5	AAE21092 Human IL-
70	207.5	10.7	488	5	AAE21092 Human IL-
71	207.5	10.7	488	5	AAE21092 Human IL-
72	207.5	10.7	488	5	AAE21092 Human IL-
73	207.5	10.7	488	5	AAE21092 Human IL-
74	207.5	10.7	488	5	AAE21092 Human IL-
75	199.5	10.3	708	2	AAE21092 Human IL-
76	196	10.1	36	4	AAE21092 Human IL-
77	186.5	9.6	837	8	AAE21092 Human IL-
78	186.5	9.6	837	8	AAE21092 Human IL-
79	182.5	9.4	837	8	AAE21092 Human IL-
80	182	9.4	837	8	AAE21092 Human IL-
81	182	9.4	837	8	AAE21092 Human IL-
82	182	9.4	837	8	AAE21092 Human IL-
83	182	9.4	837	8	AAE21092 Human IL-
84	182	9.4	837	8	AAE21092 Human IL-
85	182	9.4	837	8	AAE21092 Human IL-
86	182	9.4	837	8	AAE21092 Human IL-
87	181	9.4	837	8	AAE21092 Human IL-
88	181	9.4	837	8	AAE21092 Human IL-
89	177.5	9.2	1001	2	AAE21092 Human IL-
90	177	9.2	1001	2	AAE21092 Human IL-
91	174	9.0	1001	2	AAE21092 Human IL-
92	172.5	8.9	984	2	AAE21092 Human IL-
93	170	8.8	783	2	AAE21092 Human IL-
94	170	8.8	783	2	AAE21092 Human IL-
95	170	8.8	783	2	AAE21092 Human IL-
96	170	8.8	783	2	AAE21092 Human IL-
97	170	8.8	783	2	AAE21092 Human IL-

98 170 8.8 801 2 AAR11742
 99 170 8.8 814 4 AAR30069
 100 170 8.8 824 4 AAR23678

AAR11742 Clone 25-
 AAR30069 Novel hum
 AAR23678 Human Bst

ALIGNMENTS

RESULT 1

AAE24035
 ID AAE24035 standard; protein; 356 AA.

AC AAE24035;

DT 23-SEP-2002 (first entry)

DE Human haematopoietin receptor_2 (HPR2) ex9 protein.

Human haematopoietin receptor; receptor; HPR1; HPR2; cell proliferation;
 pancytopenia; leukopenia; anaemia; thrombocytopenia; osteoporosis;
 neurodegenerative disorder; leukaemia; carcinoma; haematologic disorder;
 cancer; myelodysplastic syndrome; idiopathic thrombocytopenic purpura;
 ITP; sickle cell vasocclusive crisis; myelofibrosis; myeloid metaplasia;
 osteoclast disorder; periodontitis; acute polyneuropathy; Bell's palsy;
 anorexia nervosa; chronic fatigue syndrome; Creutzfeldt-Jacob disease;
 demyelinating neuropathy; Guillain-Barre syndrome; Gulf war syndrome;
 vertebral disc disease; myaesthesia gravis; chronic neuronal degeneration;
 stroke; fatigue; tumour; sarcoma; osteoporosis; obesity; infertility;
 ischaemic disease.

OS Homo sapiens.

FN WO200229060-A2.

PD 11-APR-2002.

PF 05-OCT-2001; 2001WO-US031634.

PR 06-OCT-2000; 2000US-0238706P.

PR 13-OCT-2000; 2000US-0240476P.

PR 20-FEB-2001; 2001US-0270282P.

PA (IMMV) IMMUNEX CORP.

PI Coeman DJ, Mosley BA, Bird TA, Dubose RF, Wiley SR,

DR WPI; 2002-330172/36.

PT N-PSDB; AAD38775.

PS Human and murine haematopoietin receptor polypeptides HPR1 and HPR2,
 useful for treating cell proliferation, metabolic, and reproductive
 hormone related conditions.

XX Claim 3; Page 127-129; 136p; English.

XX The present invention relates to human and murine haematopoietin receptor
 CC polypeptides HPR1 and HPR2. Sequences of the invention are useful for
 CC treating cell proliferation conditions e.g., pancytopenia, leukopenia,
 CC anaemia, thrombocytopenia, neurodegenerative disorders and osteoporosis
 CC resulting from a lack of bone-forming cells. They are also useful for
 CC treating cell proliferation conditions such as leukaemia and tumour
 CC metastasis, osteoporosis resulting from an excess of bone-resorbing
 CC cells. HPR sequences are also useful for treating medical conditions and
 CC diseases such as cell proliferation, metabolic and reproductive hormone
 CC related conditions. They are useful for treating various haematologic and
 CC oncologic disorders e.g., Epstein-Barr virus-positive nasopharyngeal
 CC carcinoma, myelogenous leukemia, colon, stomach, prostate, renal cell,
 CC cervical and ovarian cancers, lung cancer (SCLC and NSCLC), including
 CC cancer-associated cachexia, fatigue, solid tumours (e.g., osteosarcoma,
 CC squamous cell carcinoma (e.g., adenocarcinoma (for example, breast cancer),
 CC sarcoma), carcinoma), haematologic disorders, anaemias (e.g., anaemia
 CC of chronic disease, aplastic anaemia, Fanconi's aplastic anaemia), myelo-
 CC dysplastic syndromes (including refractory anaemia, refractory anaemia

CC with ringed sideroblasts or with excess blasts), idiopathic thrombocyto-
 CC paenic purpura (ITP), sickle cell vasocclusive crisis, myelofibrosis/
 CC myeloid metaplasia, osteoclast disorders that lead to bone loss such as
 CC osteoporosis including post-menopausal osteoporosis, periodontitis
 CC resulting in tooth loosening or loss, prosthesis loosening after joint
 CC replacement, neurodegenerative conditions (e.g., acute polyneuropathy,
 CC Bell's palsy, anorexia nervosa, chronic fatigue syndrome, transmissible
 CC dementia including Creutzfeldt-Jacob disease, demyelinating neuropathy,
 CC Guillain-Barre syndrome, vertebral disc disease, Gulf war syndrome,
 CC myaesthesia gravis, chronic neuronal degeneration, stroke including
 CC cerebral ischaemic diseases. HPR1 and HPR2 polypeptides are also useful
 CC for treating various other disorders such as osteoporosis, obesity,
 CC deficient mammary development and infertility. The present sequence is
 CC human HPR2 ex9 protein

XX Sequence 356 AA;

Query Match 100.0%; Score 1934; DB 5; Length 356;

Best Local Similarity 100.0%; Pred. No. 4,1e-162;

Matches 356; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNQVTTQMDAVIALYILFSKCHGTTNINCSGHVWEPAITFKMGMINISYCOAIIKNCQ 60
 DB 1 MNQVTTQMDAVIALYILFSKCHGTTNINCSGHVWEPAITFKMGMINISYCOAIIKNCQ 60
 QY 61 PRKLFYKNGIKERQITRIKKTARLWYKPLFEPHASMCTACGCKHPOETLLIGKDIS 120
 DB 61 PRKLFYKNGIKERQITRIKKTARLWYKPLFEPHASMCTACGCKHPOETLLIGKDIS 120
 QY 121 SGYPPIIDPEVTCVIEYSGNMTCTMNAKLTLYIDTKYVHVKSLETSEBOQYLTSSYIN 180
 DB 121 SGYPPIIDPEVTCVIEYSGNMTCTMNAKLTLYIDTKYVHVKSLETSEBOQYLTSSYIN 180
 QY 181 ISTDSLGQSKYLVWVQANALGMESKQLOIHLDDIYIPSAVYSRAETINATYPKTII 240
 DB 181 ISTDSLGQSKYLVWVQANALGMESKQLOIHLDDIYIPSAVYSRAETINATYPKTII 240
 QY 241 YWDSOTTEKXSCERYKATNTQTNVKEPDPNFTYVOOSELYLPNIRKYVQVCOENG 300
 DB 241 YWDSOTTEKXSCERYKATNTQTNVKEPDPNFTYVOOSELYLPNIRKYVQVCOENG 300
 QY 301 KRYWQMSLSFPHKTPETVPQVTSKAFQHDITNSGLTVASISTGHLTSGLKSGSYC 356
 DB 301 KRYWQMSLSFPHKTPETVPQVTSKAFQHDITNSGLTVASISTGHLTSGLKSGSYC 356

RESULT 2

AAE24035
 ID AAE24035 standard; protein; 428 AA.

AC AAE24035;

DT 11-JUL-2001 (first entry)

DE Human haematopoietin receptor protein NR12.4 SEQ ID NO:8.

XX Human, haematopoietin receptor protein, NR12; immunosuppressive;
 CC antiallergic; haematopoietin factor; autoimmune disease; tissue
 CC metal allergy; pollen allergy.

OS Homo sapiens.

FN WO200123556-A1.

PD 05-APR-2001.

PF 27-SEP-2000; 2000WO-JP006654.

PR 27-SEP-1999; 99JP-00273358.

PR 03-AUG-2000; 2000JP-00240397.

PA (CHUGAI) CHUGAI RES INST MOLECULAR MEDICINE INC.

XX

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: April 3, 2006, 08:22:56 ; Search time 99.9157 Seconds
(without alignments)
2513.799 Million cell updates/sec

Title: US-10-715-667-25

Sequence: 1 MNOVTIQMDVAVLALYILPSM.....TVASISTGHLTSGLKRGSTYC 356

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 segs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Uniprot_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1888	97.6	629	05VWK5_HUMAN	05VWK5 homo sapien
2	1881	97.3	629	08NFO9_HUMAN	08NFO9 homo sapien
3	1720	88.9	320	04VGP1_HUMAN	04VGP1 homo sapien
4	1701	88.0	320	04VGP3_HUMAN	04VGP3 homo sapien
5	1674	86.6	593	04VGP6_HUMAN	04VGP6 homo sapien
6	1421.5	73.5	644	08K4B4_MOUSE	08K4B4 mus musculus
7	705	36.5	138	04VGP5_HUMAN	04VGP5 homo sapien
8	511	26.4	375	04VGP4_HUMAN	04VGP4 homo sapien
9	449	23.2	390	05VWK7_HUMAN	05VWK7 homo sapien
10	442	22.9	391	096AS1_HUMAN	096AS1 homo sapien
11	329.5	17.0	869	05GR16_CHICK	05GR16 gallus galli
12	281.5	14.6	918	09W6U9_CHICK	09W6U9 gallus galli
13	277	14.3	554	06UN2_TETNG	06UN2 tetraodon n
14	261.5	13.5	917	IL6RB_MOUSE	IL6RB mus musculus
15	261.5	13.5	917	06PD19_MOUSE	06PD19 mus musculus
16	253.5	13.0	874	IL2R2_MOUSE	IL2R2 mus musculus
17	252	13.0	861	IL2R2_BOVIN	IL2R2 bos taurus
18	246.5	12.7	881	057515_XENLA	057515 xenopus lae
19	245.5	12.7	1010	07T089_RAT	07T089 rattus norv
20	240.5	12.4	813	06UN1_TETNG	06UN1 tetraodon n
21	230.5	11.9	918	IL6RB_RAT	IL6RB rattus norv
22	230	11.9	858	04OYCB_CANPA	04OYCB canis faml
23	223	11.5	861	IL2R2_PIG	IL2R2 sus scrofa
24	222	11.5	862	IL2R2_HUMAN	IL2R2 homo sapien
25	222	11.5	862	05VWK8_HUMAN	05VWK8 homo sapien
26	212.5	11.0	918	IL6RB_HUMAN	IL6RB homo sapien
27	211.5	10.9	857	05FC04_HUMAN	05FC04 homo sapien
28	211	10.9	2030	04S3E8_TETNG	04S3E8 tetraodon n
29	197.5	10.2	813	06DD37_XENLA	06DD37 xenopus lae
30	189	9.8	394	06UNO5_TETNG	06UNO5 tetraodon n
31	187	9.7	1097	05XMR9_CANPA	05XMR9 canis faml

32	186.5	9.6	837	1	CSFR_MOUSE	P40223 mus musculus
33	186	9.6	477	2	05F3Y5_CHICK	05F3Y5 gallus galli
34	182	9.4	1097	1	LIFR_HUMAN	P42702 homo sapien
35	178.5	9.2	739	2	04T141_TETNG	04T141 tetraodon n
36	178.5	9.2	870	2	06UNO_TETNG	06UNO tetraodon n
37	175	9.0	617	2	07SS21_RANCA	07SS21 rana catesb
38	172	8.9	389	2	06DG28_BRARE	06DG28 brachydanio
39	170	8.8	836	1	CSFR3_HUMAN	099062 homo sapien
40	168	8.7	719	2	0510Y2_MOUSE	0510Y2 mus musculus
41	168	8.7	1092	1	LIFR_MOUSE	P42703 mus musculus
42	167	8.6	425	1	CRLE1_MOUSE	09Jm58 mus musculus
43	162.5	8.4	422	1	CRLE1_HUMAN	075462 homo sapien
44	161.5	8.4	582	2	06UML6_HUMAN	06UML6 homo sapien
45	161.5	8.4	764	2	06EBC4_HUMAN	06EBC4 homo sapien
46	161	8.3	1093	2	070535_RAT	070535 rattus norv
47	158	8.2	324	2	06EBC5_HUMAN	06EBC5 homo sapien
48	158	8.2	509	2	08WYJ0_HUMAN	08WYJ0 homo sapien
49	158	8.2	649	2	06EBC6_HUMAN	06EBC6 homo sapien
50	158	8.2	662	2	06EBC3_HUMAN	06EBC3 homo sapien
51	158	8.2	732	2	08N117_HUMAN	08N117 homo sapien
52	158	8.2	819	2	0616F7_EUBMA	0616F7 eublepharis
53	153	7.9	229	2	05VWK6_HUMAN	05VWK6 homo sapien
54	151.5	7.8	547	2	06EAL6_MOUSE	06EAL6 mus musculus
55	151.5	7.8	662	2	06EAL7_MOUSE	06EAL7 mus musculus
56	151.5	7.8	716	2	08K5B1_MOUSE	08K5B1 mus musculus
57	151.5	7.8	716	2	08R501_MOUSE	08R501 mus musculus
58	151.5	7.8	1148	2	091BA7_CHICK	091BA7 gallus galli
59	150.5	7.8	334	2	06UC85_CHICK	06UC85 gallus galli
60	150.5	7.8	492	2	06NZF0_MOUSE	06NZF0 mus musculus
61	150.5	7.8	1148	2	0918V6_CHICK	0918V6 gallus galli
62	150	7.8	622	2	0865V4_CEBAP	0865V4 cebus aelli
63	147	7.6	288	2	096P36_HUMAN	096P36 homo sapien
64	147	7.6	349	2	090HJ5_HUMAN	090HJ5 homo sapien
65	147	7.6	376	2	096P35_HUMAN	096P35 homo sapien
66	147	7.6	581	1	PRLR_BOVIN	028172 bos taurus
67	147	7.6	622	1	PRLR_HUMAN	P16471 homo sapien
68	147	7.6	622	1	05RAN0_PONPY	05RAN0 pongo pygma
69	146.5	7.6	437	2	04RMP5_TETNG	04RMP5 tetraodon n
70	146.5	7.6	604	2	08QG54_CYPCA	08QG54 cyprinus ca
71	145.5	7.5	1147	2	09DDK1_MELGA	09DDK1 melagris g
72	143	7.4	581	1	PRLR_SHEEP	046561 ovis aries
73	142.5	7.4	602	2	06UN22_BRARE	06UN22 brachydanio
74	142	7.3	600	2	09PTP0_CARAU	09PTP0 carassius a
75	141.5	7.3	622	2	09N0U7_CALJA	09N0U7 callitrich
76	141.5	7.3	831	1	PRLR_CHICK	090459 gallus galli
77	141.5	7.3	831	2	06ODAO_CHICK	06ODAO gallus galli
78	140.5	7.3	460	2	07T220_CHICK	07T220 gallus galli
79	140	7.2	268	2	08TD78_HUMAN	08TD78 homo sapien
80	139.5	7.2	609	2	05ISE1_CYPCA	05ISE1 cyprinus ca
81	138.5	7.2	623	1	IL2R1_MOUSE	IL2R1 mus musculus
82	136	7.0	360	2	06UPA0_TETNG	06UPA0 tetraodon n
83	136	7.0	818	2	0640Q2_MOUSE	0640Q2 mus musculus
84	136	7.0	1165	1	LEBR_MOUSE	P48571 mus musculus
85	136	7.0	1165	1	LEBR_PIG	002571 sus scrofa
86	136	7.0	1166	2	04W810_CANPA	04W810 canis faml
87	133	6.9	659	2	04G138_HUMAN	04G138 homo sapien
88	132.5	6.9	346	2	093404_OREMO	093404 oreochromis
89	132	6.8	881	2	0642Z2_MYOLU	0642Z2 myotis lucif
90	132	6.8	1153	2	05XXB8_MYOLU	05XXB8 myotis lucif
91	131.5	6.8	831	1	PRLR_MELGA	091094 melagris g
92	131	6.8	1165	1	LEBR_HUMAN	P48357 homo sapien
93	130	6.7	283	2	06UCB4_CHICK	06UCB4 gallus galli
94	130	6.7	581	1	PRLR_CEREL	028355 cervus elap
95	130	6.7	1162	1	LEBR_RAT	062859 rattus norv
96	129.5	6.7	894	2	06UNM7_TETNG	06UNM7 tetraodon n
97	127.5	6.6	227	2	09GLM3_URSMA	09GLM3 ursus marit
98	126.5	6.5	830	1	PRLR_COLL	090374 columba liv
99	126.5	6.5	1083	2	08QF07_CHICK	08QF07 gallus galli
100	125.5	6.5	310	2	058DZ7_RAT	058DZ7 rattus norv

ALIGNMENTS

```
RESULT 1
OSVWKS_HUMAN
ID OSVWKS_HUMAN PRELIMINARY; PRT; 629 AA.
AC OSVWKS;
DT 01-FEB-2005 (TREMBlrel. 29, Created)
DT 01-FEB-2005 (TREMBlrel. 29, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE Interleukin 23 receptor.
GN Name=IL23R; ORFNames=Rpl1-131015.1-001;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall R.;
RL Submitted (May-2005) to the EMBL/GenBank/DBJ databases.
RP NUCLEOTIDE SEQUENCE.
RA Davidson C.;
RL Submitted (May-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL389925; CAH70406.1; -; Genomic DNA.
DR EMBL; AL109843; CAI22678.1; -; Genomic DNA.
DR EMBL; AL109843; CAH70406.1; JOINED; Genomic DNA.
DR EMBL; AL389925; CAI22678.1; JOINED; Genomic DNA.
DR HGNC; HGNC:19100; IL23R.
DR GO; GO:0016021; C:Integral to membrane, IEA.
DR GO; GO:0004872; F:receptor activity, IEA.
DR InterPro; IPR003961; FN_III.
DR Pfam; PF00041; FN3; 1.
DR PROSITE; PS50853; FN3; 2.
KW Receptor; Repeat; Transmembrane.
SQ SEQUENCE 629 AA; 71722 MW; AC63C89B81AABF05 CRC64;

Query Match 97.6%; Score 1888; DB 2; Length 629;
Best Local Similarity 100.0%; Pred. No. 7,4e-141;
Matches 348; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNQVTTQMDAVIALYILFSWCHGGITNINCSGHIWVEPATIFPKGMNISIYCOAIRKQ 60
DB 1 MNQVTTQMDAVIALYILFSWCHGGITNINCSGHIWVEPATIFPKGMNISIYCOAIRKQ 60
QY 61 PRKHAFYNGIKERFOITRIKKTARLWYKNFLBPHASMYCTACBPKHFOETLLCGKD 120
DB 61 PRKHAFYNGIKERFOITRIKKTARLWYKNFLBPHASMYCTACBPKHFOETLLCGKD 120
QY 121 SGYPDPIDPEYTCVLYEYSGMNTCTWNAKLTLYIDTKVVAHVKSLETEBOOYLTSYIN 180
DB 121 SGYPDPIDPEYTCVLYEYSGMNTCTWNAKLTLYIDTKVVAHVKSLETEBOOYLTSYIN 180
QY 181 ISTSLQGGKKYLWVQAAANLGMESKQLOIHLDIVIPSAAVISRATTINATVPKTI 240
DB 181 ISTSLQGGKKYLWVQAAANLGMESKQLOIHLDIVIPSAAVISRATTINATVPKTI 240
QY 241 YMSQTTIEKYSCEMRKYATTNQTNVKEPDTNFTYVQOSEFYLEPNIKYFVQRQCE 300
DB 241 YMSQTTIEKYSCEMRKYATTNQTNVKEPDTNFTYVQOSEFYLEPNIKYFVQRQCE 300
QY 301 KRYQPMSSLPFHKTPTETVPQVTSKAFQHDWTNSGLTVASISTGHLTS 348
DB 301 KRYQPMSSLPFHKTPTETVPQVTSKAFQHDWTNSGLTVASISTGHLTS 348

RESULT 2
OSNFO9_HUMAN
ID OSNFO9_HUMAN PRELIMINARY; PRT; 629 AA.
AC OSNFO9;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Interleukin-23 receptor.
```

```
GN Name=IL23R; Synonyms=IL-23R;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Parham C., Chirica M., Timans J., Vaisberg E., Travle M., Cheung J.,
RA Pflanz S., Zhang R., Singh K.P., Vega F., To W., Wagner U.,
RA O'Farrell A.-M., McClanahan T., Zurawski S., Hannum C., Gorman D.,
RA Remick D.M., Kastelein R.A., de Waal Malefyt R., Moore K.W.;
RT "A receptor for the heterodimeric cytokine IL-23 is composed of IL-
RT 12beta1 and a novel cytokine receptor subunit, IL-23R."
J. Immunol. 168:5699-5708(2002).
RL J. Immunol. 168:5699-5708(2002).
DR EMBL; AF461422; AAM44229.1; -; mRNA.
DR HSSP; P16471; 1BP3.
DR Ensembl; ENSG00000162594; Homo sapiens.
DR HGNC; HGNC:19100; IL23R.
DR GO; GO:0004872; F:receptor activity, IEA.
DR InterPro; IPR003961; FN_III.
DR Pfam; PF00041; FN3; 1.
DR SMART; SM00060; FN3; 1.
DR PROSITE; PS50853; FN3; 2.
KW Receptor.
SQ SEQUENCE 629 AA; 71706 MW; C4228CDA7C6B425 CRC64;

Query Match 97.3%; Score 1881; DB 2; Length 629;
Best Local Similarity 99.7%; Pred. No. 2,7e-140;
Matches 347; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNQVTTQMDAVIALYILFSWCHGGITNINCSGHIWVEPATIFPKGMNISIYCOAIRKQ 60
DB 1 MNQVTTQMDAVIALYILFSWCHGGITNINCSGHIWVEPATIFPKGMNISIYCOAIRKQ 60
QY 61 PRKHAFYNGIKERFOITRIKKTARLWYKNFLBPHASMYCTACBPKHFOETLLCGKD 120
DB 61 PRKHAFYNGIKERFOITRIKKTARLWYKNFLBPHASMYCTACBPKHFOETLLCGKD 120
QY 121 SGYPDPIDPEYTCVLYEYSGMNTCTWNAKLTLYIDTKVVAHVKSLETEBOOYLTSYIN 180
DB 121 SGYPDPIDPEYTCVLYEYSGMNTCTWNAKLTLYIDTKVVAHVKSLETEBOOYLTSYIN 180
QY 181 ISTSLQGGKKYLWVQAAANLGMESKQLOIHLDIVIPSAAVISRATTINATVPKTI 240
DB 181 ISTSLQGGKKYLWVQAAANLGMESKQLOIHLDIVIPSAAVISRATTINATVPKTI 240
QY 241 YMSQTTIEKYSCEMRKYATTNQTNVKEPDTNFTYVQOSEFYLEPNIKYFVQRQCE 300
DB 241 YMSQTTIEKYSCEMRKYATTNQTNVKEPDTNFTYVQOSEFYLEPNIKYFVQRQCE 300
QY 301 KRYQPMSSLPFHKTPTETVPQVTSKAFQHDWTNSGLTVASISTGHLTS 348
DB 301 KRYQPMSSLPFHKTPTETVPQVTSKAFQHDWTNSGLTVASISTGHLTS 348

RESULT 3
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ID Q4VGP1_HUMAN PRELIMINARY; PRT; 320 AA.
AC Q4VGP1;
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE Interleukin 23 receptor isoform 4 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Zhang X.-Y., Zhang Y., Zhang H.-D., Wang S.-H., Liu L.;
```

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 3, 2006, 08:24:45 ; Search time 15.0008 Seconds
(without alignments)
1962.071 Million cell updates/sec

Title: US-10-715-667-25

Sequence: 1 MNOVTIQMDAVIALYILPSM.....TVASISTGHTLSGLKRGSYC 356

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/prodata/1/1aa/5_COMB.pep:*
- 2: /cgn2_6/prodata/1/1aa/6_COMB.pep:*
- 3: /cgn2_6/prodata/1/1aa/H_COMB.pep:*
- 4: /cgn2_6/prodata/1/1aa/PCITUS_COMB.pep:*
- 5: /cgn2_6/prodata/1/1aa/RE_COMB.pep:*
- 6: /cgn2_6/prodata/1/1aa/backfilest1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1868	96.6	629	2	US-09-853-180B-2
2	222	11.5	862	1	US-08-685-118-2
3	222	11.5	862	1	US-08-915-495-2
4	222	11.5	862	1	US-08-914-520-2
5	222	11.5	862	2	US-09-853-180B-4
6	222	11.5	864	2	US-09-949-016-7758
7	215.5	11.1	859	2	US-09-313-942-7
8	215.5	11.1	859	2	US-10-282-162-7
9	215.5	11.1	951	2	US-09-313-942-9
10	215.5	11.1	951	2	US-10-282-162-9
11	213	11.0	332	2	US-09-313-942-10
12	213	11.0	332	2	US-10-282-162-10
13	212.5	11.0	658	1	US-08-825-558-4
14	212.5	11.0	658	2	US-09-312-611-4
15	212.5	11.0	918	1	US-08-825-558-6
16	212.5	11.0	918	2	US-09-312-611-6
17	212.5	11.0	918	2	US-09-853-180B-3
18	212.5	11.0	918	2	US-09-949-002-333
19	211.5	10.9	708	1	US-07-797-556-2
20	211.5	10.9	708	1	US-08-308-881-2
21	211.5	10.9	708	1	US-09-058-263-2
22	211.5	10.9	708	1	US-09-059-099-2
23	211.5	10.9	708	2	US-09-058-264-2
24	211.5	10.9	708	2	US-09-455-962-2
25	211.5	10.9	708	4	PCR-US95-06530-2
26	211.5	10.9	937	2	US-09-949-002-536
27	207.5	10.7	488	1	US-08-599-455B-5

28	207.5	10.7	488	2	US-09-069-781B-5	Sequence 5, App11
29	207.5	10.7	488	2	US-09-137-132-5	Sequence 5, App11
30	207.5	10.7	488	2	US-08-864-564A-5	Sequence 5, App11
31	207.5	10.7	488	2	US-09-094-410-5	Sequence 5, App11
32	207.5	10.7	488	2	US-08-708-123D-5	Sequence 5, App11
33	207.5	10.7	488	2	US-08-583-153A-5	Sequence 5, App11
34	207.5	10.7	488	2	US-08-638-524B-5	Sequence 5, App11
35	207.5	10.7	1158	2	US-09-313-942-26	Sequence 26, App1
36	207.5	10.7	1158	2	US-10-282-162-26	Sequence 26, App1
37	207.5	10.7	1168	2	US-09-313-942-24	Sequence 24, App1
38	207.5	10.7	1168	2	US-10-282-162-24	Sequence 24, App1
39	186.5	9.6	837	1	US-07-923-976-2	Sequence 2, App11
40	182	9.4	1001	1	US-07-923-976-6	Sequence 6, App11
41	182	9.4	1001	1	US-07-943-843-2	Sequence 2, App11
42	182	9.4	1001	1	US-08-347-003-2	Sequence 2, App11
43	182	9.4	1097	1	US-07-943-843-6	Sequence 6, App11
44	182	9.4	1097	1	US-08-347-003-6	Sequence 6, App11
45	182	9.4	1097	2	US-09-949-016-6209	Sequence 6209, App
46	182	9.4	1119	2	US-09-949-016-10081	Sequence 10081, App
47	170	8.8	771	1	US-07-923-976-6	Sequence 6, App11
48	170	8.8	783	6	542248-2	Patent No. 542248
49	170	8.8	836	1	US-07-923-976-4	Sequence 4, App11
50	170	8.8	863	1	US-07-923-976-8	Sequence 8, App11
51	168	8.7	620	1	US-08-419-652-7	Sequence 7, App11
52	168	8.7	719	1	US-07-943-843-4	Sequence 4, App11
53	168	8.7	719	1	US-08-347-003-4	Sequence 4, App11
54	167	8.6	385	2	US-09-071-224-19	Sequence 19, App1
55	167	8.6	405	2	US-09-012-072-2	Sequence 2, App11
56	167	8.6	425	2	US-09-120-601-2	Sequence 2, App11
57	167	8.6	405	2	US-09-071-224-6	Sequence 6, App11
58	166.5	8.6	572	1	US-08-419-652-5	Sequence 5, App11
59	163.5	8.5	303	2	US-09-071-224-21	Sequence 21, App1
60	163.5	8.5	389	2	US-09-071-224-24	Sequence 24, App1
61	163.5	8.5	389	2	US-09-071-224-27	Sequence 27, App1
62	163.5	8.5	389	2	US-09-071-224-29	Sequence 29, App1
63	163.5	8.5	422	2	US-09-071-224-2	Sequence 2, App11
64	163	8.4	407	2	US-09-521-335-13	Sequence 13, App1
65	162.5	8.4	303	2	US-09-071-224-23	Sequence 23, App1
66	162.5	8.4	385	2	US-09-071-224-20	Sequence 20, App1
67	162.5	8.4	388	2	US-09-071-224-17	Sequence 17, App1
68	162.5	8.4	389	2	US-09-071-224-22	Sequence 22, App1
69	162.5	8.4	389	2	US-09-071-224-26	Sequence 26, App1
70	162.5	8.4	392	2	US-09-071-224-18	Sequence 18, App1
71	162.5	8.4	410	2	US-09-521-335-12	Sequence 12, App1
72	162.5	8.4	422	2	US-09-866-028-32	Sequence 32, App1
73	162.5	8.4	422	2	US-09-944-457-32	Sequence 32, App1
74	162.5	8.4	422	2	US-09-945-584-33	Sequence 33, App1
75	162.5	8.4	422	2	US-09-944-944-32	Sequence 32, App1
76	162.5	8.4	422	2	US-09-945-587-32	Sequence 32, App1
77	162.5	8.4	425	2	US-09-071-224-4	Sequence 4, App11
78	162.5	8.4	434	2	US-09-012-072-4	Sequence 4, App11
79	162.5	8.4	434	2	US-09-120-601-4	Sequence 4, App11
80	162.5	8.4	448	2	US-09-120-601-6	Sequence 6, App11
81	161.5	8.4	389	2	US-09-071-224-28	Sequence 28, App1
82	161.5	8.4	389	2	US-09-071-224-30	Sequence 30, App1
83	160.5	8.3	389	2	US-09-071-224-31	Sequence 31, App1
84	159.5	8.2	389	2	US-09-071-224-25	Sequence 25, App1
85	150.5	7.8	602	1	US-08-419-652-6	Sequence 6, App11
86	147	7.6	349	2	US-08-806-597A-14	Sequence 14, App1
87	147	7.6	349	2	US-08-970-428B-14	Sequence 14, App1
88	147	7.6	599	2	US-09-000-145-2	Sequence 2, App11
89	147	7.6	637	2	US-09-949-016-10128	Sequence 10128, App11
90	138.5	7.2	623	1	US-08-653-740-7	Sequence 7, App11
91	138.5	7.2	623	1	US-09-073-594-7	Sequence 7, App11
92	138.5	7.2	623	1	US-09-275-925-7	Sequence 7, App11
93	136	7.0	894	2	US-08-599-455B-2	Sequence 2, App11
94	136	7.0	894	2	US-09-069-781B-2	Sequence 2, App11
95	136	7.0	894	2	US-08-618-957A-12	Sequence 12, App1
96	136	7.0	894	2	US-09-137-132-2	Sequence 2, App11
97	136	7.0	894	2	US-08-864-564A-2	Sequence 2, App11
98	136	7.0	894	2	US-09-094-410-2	Sequence 2, App11
99	136	7.0	894	2	US-08-708-123D-2	Sequence 2, App11
100	136	7.0	894	2	US-08-583-153A-2	Sequence 2, App11

